

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 4, 2002, 16:15:58 ; Search time 172.18 Seconds  
(without alignments)  
221.041 Million cell updates/sec

Title: US-09-052-089a-3  
Perfect score: 1066  
Sequence: 1 RTIINKLFFDLAEEENVLD.....DLQSDAKKEIMSLKKRLTMLQ 220

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_19:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriapi:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1066	100.0	469	4	000467
2	1046	98.1	469	4	Q9BWF2
3	919	86.2	470	11	Q9CNP4
4	919	86.2	470	11	Q08854
5	654	61.4	233	11	Q922M8
6	530	49.7	433	13	Q9YGN2
7	178	16.7	1958	5	Q96062
8	167	15.7	529	4	Q9UP81
9	167	15.7	948	4	Q9UIK7
10	167	15.7	2473	11	Q9Q284
11	165	15.5	1092	13	Q90338
12	165	15.5	1578	10	Q9AV25
13	165	15.5	1931	13	Q42352
14	164.5	15.4	324	11	Q9Q9N8
15	164	15.4	692	5	Q96720
16	164	15.4	1530	4	Q43241

17	163	15.3	1933	13	Q90337	Q90337 cyprinus ca
18	162	15.2	976	11	Q99M12	Q99M12 mus musculu
19	162	15.2	1120	11	Q99M11	Q99M11 mus musculu
20	162	15.2	1743	5	Q96063	Q96063 dugesia jap
21	162	15.2	1930	13	Q9DGD5	Q9DGD5 pennahia ar
22	161	15.1	1447	11	Q9QYT2	Q9QYT2 mus musculu
23	161	15.1	1487	11	Q9QYT3	Q9QYT3 mus musculu
24	160.5	15.1	876	5	Q9BWM8	Q9BWM8 sarcopites s
25	160.5	15.1	1219	5	Q9NJ23	Q9NJ23 aequipecten
26	160.5	15.1	2168	11	Q61043	Q61043 mus musculu
27	160	15.0	435	5	Q95S85	Q95S85 drosophila
28	159.5	15.0	1229	5	Q9NJ22	Q9NJ22 aequipecten
29	159.5	15.0	1243	5	Q9NJ21	Q9NJ21 aequipecten
30	159.5	15.0	1253	3	Q9NJ20	Q9NJ20 aequipecten
31	159.5	15.0	1951	5	Q17042	Q17042 aequipecten
32	159.5	15.0	2139	5	Q07569	Q07569 entamoeba h
33	159	14.9	1790	3	Q07380	Q07380 saccharomyc
34	159	14.9	1939	6	Q9TW61	Q9TW61 sus scrofa
35	158.5	14.9	1941	5	Q26079	Q26079 placopeten
36	156.5	14.7	786	13	Q91520	Q91520 thunnus thy
37	156.5	14.7	1138	5	Q22276	Q22276 caenorhabdi
38	156.5	14.7	1940	5	Q9U7E3	Q9U7E3 pecten maxi
39	155.5	14.6	959	11	Q91WE7	Q91WE7 mus musculu
40	155.5	14.6	1164	5	P92021	P92021 caenorhabdi
41	155.5	14.6	1205	5	Q967H0	Q967H0 caenorhabdi
42	155.5	14.6	1935	5	Q44934	Q44934 loligo peal
43	155.5	14.6	1938	13	Q91BD7	Q91BD7 seriola dum
44	155	14.5	1455	5	Q9V8D7	Q9V8D7 drosophila
45	155	14.5	1119	13	P87344	P87344 theragra ch

## ALIGNMENTS

RESULT 1  
ID 000467 PRELIMINARY: PRT: 469 AA.  
AC 000467;  
DT 01-JUL-1997 (TREMBLrel. 04, Created)  
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)  
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DI HTRIP.  
GN HTRIP.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RM  
SEQUENCE FROM N.A.  
RX MEDLINE=97258620; PubMed=9104814;  
RA Lee S.Y., Lee S.Y., Choi Y.;  
RT "TRAF-interacting protein (TRIP): a novel component of the tumor  
RT necrosis factor receptor (TNFR)- and CD30-TRAF signaling complexes  
RT that inhibits TRAF2-mediated NF-kappaB activation.";  
RC J. Exp. Med. 185:1275-1285(1997).  
- 1. SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
DR EMBL: U77845; AAB52993.1; -  
DR InterPro: IPR001841; ZnfC1ng.  
DR Pfam: PF00097; zf-C3HC4; 1.  
DR SMART: SM00184; RING; 1.  
KW Zinc-finger.  
SQ SEQUENCE 469 AA; 53138 MW; 2D54ED04B84ABAE4 CRC64;

Query Match 100.0%; Score 1066; DB 4; Length 469;  
Best Local Similarity 100.0%; Pred. No. 1,le-52;  
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTIINKLFFDLAEEENVLDREFLKNELNDVRAQLSQDKERKRSQVITIDRLPTLEERN 60  
DB 56 RTIINKLFFDLAEEENVLDREFLKNELNDVRAQLSQDKERKRSQVITIDRLPTLEERN 115  
QY 61 ATVVSLOALGKAEMLSTLKKQMKYLEQOQDETQAOEAGRLRSKKMTMEQIELLQS 120

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Db 116 ATVVSILQALKAEMLCSTLKKOMKYLEQODETKQAOEAGRLSKKMTMEQIEILLQS 175
QY 121 QLPVEEEMIRMGVQGSQAVEQOLAVYCVSLKKEYENLKARRKASGEVADKLKRDLFSSRSK 180
Db 176 QLPVEEEMIRMGVQGSQAVEQOLAVYCVSLKKEYENLKARRKASGEVADKLKRDLFSSRSK 235
QY 181 LQTVYSELDAQKLELSAQKDLQSDAKDEIMSLKKLTMLQ 220
Db 236 LQTVYSELDAQKLELSAQKDLQSDAKDEIMSLKKLTMLQ 275

RESULT 2
09BWF2 PRELIMINARY: PRT: 469 AA.
AC 09BWF2:
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE TRAF INTERACTING PROTEIN.
OC Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN 11
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG CARCINOMA;
RA Strausberg R.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; BC000310; AAH00310.1; -.
DR InterPro: IPR001841; Znf_Fing.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00184; RING; 1.
KW Zinc-finger.
SQ SEQUENCE 469 AA; 53294 MW; B9EF3808FBC5985B CRC64;

Query Match 98.1%; Score 1046; DB 4; Length 469;
Best Local Similarity 98.6%; Pred. No. 1.4e-51;
Matches 217; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EMBRYO;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aikawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batlow S., Casavant T.,
RA Fleschmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staabli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; AK012948; BAB28567.1; -.
DR EMBL; AK012786; BAB28469.1; -.
DR MGD: MGI:1096377; Traip.
DR InterPro: IPR001841; Znf_Fing.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00184; RING; 1.
KW Zinc-finger.
SQ SEQUENCE 470 AA; 53149 MW; B9FABC49A9F4BFEZ CRC64;

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Query Match 86.2%; Score 919; DB 11; Length 470;
Best Local Similarity 85.5%; Pred. No. 1.9e-44;
Matches 188; Conservative 19; Mismatches 13; Indels 0; Gaps 0;

QY 1 RTIINKLFFDLQAEENVLDBREFLNELNDVNRQOLSQDKRKRSQVITDRLRPLEERN 60
Db 56 RTIINKLFFDLQAEENVLDBREFLNELNDVNRQOLSQDKRKRSQVITDRLRPLEERN 115
QY 61 ATVVSILQALKAEMLCSTLKKOMKYLEQODETKQAOEAGRLSKKMTMEQIEILLQS 120
Db 116 ATVVSILQALKAEMLCSTLKKOMKYLEQODETKQAOEAGRLSKKMTMEQIEILLQS 175
QY 121 QLPVEEEMIRMGVQGSQAVEQOLAVYCVSLKKEYENLKARRKASGEVADKLKRDLFSSRSK 180
Db 176 QPVEEEMIRMGVQGSQAVEQOLAVYCVSLKKEYENLKARRKASGEVADKLKRDLFSSRSK 235
QY 181 LQTVYSELDAQKLELSAQKDLQSDAKDEIMSLKKLTMLQ 220
Db 236 LQTVYSELDAQKLELSAQKDLQSDAKDEIMSLKKLTMLQ 275

RESULT 4
008854 PRELIMINARY: PRT: 470 AA.
AC 008854:
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE MTRIP.
CN TRAF OR MTRIP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 11
RP SEQUENCE FROM N.A.
RC MEDLINE=97258620; PubMed=9104814;
RA Lee S.Y., Lee S.Y., Choi Y.;
RT "TRAF-interacting protein (TRIP): a novel component of the tumor

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RT necrosis factor receptor (TNFR)- and CD30-TRAF signaling complexes  
 RT that inhibits TRAF2-mediated NF-kappaB activation.";  
 RL J. Exp. Med. 185:1275-1285(1997).  
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
 DR EMBL: U77844; AAB52994.1; -.  
 DR MGD: MGI:1096377; Tralp.  
 DR InterPro: IPR001841; Znf\_ring.  
 DR Pfam: PF00097; zf-C3HC4; 1.  
 DR SMART: SM00184; RING; 1.  
 KW Zinc-finger.  
 SQ SEQUENCE 470 AA; 53191 MW; 00FD705B52645133 CRC64;

## Query Match

Best Local Similarity 86.2%; Score 919; DB 11; Length 470;  
 Matches 188; Conservative 19; Mismatches 13; Indels 0; Gaps 0;

QY 1 RTIINKLFDDLAQEEENVLDREFLKNEIDNVRAQLSQDKRKRSQVIITDLRDLTEERN 60  
 :|||||  
 DB 56 KTIINKLFDDLAQEEENVLDREFLKNEIDSVKQLSQDKRKRSQAIITDLRDLTEERN 115  
 QY 61 ATVVSLOALGKAEMLGSLTKKOKKYLEQODETKQAQEEAGRLRSKKTMEQIELLQS 120  
 :|||||  
 DB 116 ATVESLQALNKAEMLSLTKKOKKYLEQODETKQAAREEHLRLCKKKTMEQIELLQS 175  
 QY 121 QLPVEEMIRDMGVGQSAVEQLAYCVSLKKEYENLKEARKAGEVADKLKDLFFSSRSK 180  
 :|||||  
 DB 176 QRSVEEMIRDMGVGQSAVEQLAYCVSLKKEYENLKEARKATGETLADRLKDLVSSRSK 235  
 QY 181 LQTVYSELDAQKLELSAQKDLQSAKDEIKSLKKRLMLQ 220  
 :|||||  
 DB 236 LKTLNTELDQAKLELSAQKDLQSAQDEITSLRKKLMLQ 275

## RESULT 5

Q922M8 PRELIMINARY; PRT; 223 AA.

AC Q922M8;  
 DT 01-DEC-2001 (TREMblrel. 19, Created)  
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
 DE TRAF-INTERACTING PROTEIN.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Strausberg R.;  
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BC006929; AAH06929.1; -.  
 SQ SEQUENCE 223 AA; 25584 MW; 412291C205C43071 CRC64;

## Query Match

Best Local Similarity 61.4%; Score 654; DB 11; Length 223;  
 Matches 134; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 1 RTIINKLFDDLAQEEENVLDREFLKNEIDNVRAQLSQDKRKRSQVIITDLRDLTEERN 60  
 :|||||  
 DB 56 KTIINKLFDDLAQEEENVLDREFLKNEIDSVKQLSQDKRKRSQAIITDLRDLTEERN 115  
 QY 61 ATVVSLOALGKAEMLGSLTKKOKKYLEQODETKQAQEEAGRLRSKKTMEQIELLQS 120  
 :|||||  
 DB 116 ATVESLQALNKAEMLSLTKKOKKYLEQODETKQAAREEHLRLCKKKTMEQIELLQS 175  
 QY 121 QLPVEEMIRDMGVGQSAVEQLAYCVSLK 151  
 :|||||  
 DB 176 QRSVEEMIRDMGVGQSAVEQLAYCVSLK 206

## RESULT 6

Q9YGN2

ID Q9YGN2 PRELIMINARY; PRT; 433 AA.

AC Q9YGN2;  
 DT 01-MAY-1999 (TREMblrel. 10, Created)  
 DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)  
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
 DE TRAF INTERACTING PROTEIN.  
 GN TRP.  
 OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;  
 OC Tetraodontidae; Takifugu.  
 OX NCBI\_TaxID=31033;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99148833; PubMed=10025966;  
 RA Coltage A.J., Clark M., Hawker K., Umranta Y., Wheller D., Bishop M.,  
 RA Elgar G.;  
 RT "Three receptor genes for plasmalogen related growth factors in the  
 RT genome of the puffer fish Fugu rubripes.";  
 RL FEBS Lett. 443:370-374(1999)  
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
 DR EMBL: A0010317; CA909084.1; -.  
 DR InterPro: IPR001841; Znf\_ring.  
 DR Pfam: PF00097; zf-C3HC4; 1.  
 DR SMART: SM00184; RING; 1.  
 KW Zinc-finger.  
 SQ SEQUENCE 433 AA; 49201 MW; A8C31AAA4216E8C2 CRC64;

## Query Match

Best Local Similarity 49.7%; Score 530; DB 13; Length 433;  
 Matches 104; Conservative 53; Mismatches 63; Indels 0; Gaps 0;

QY 1 RTIINKLFDDLAQEEENVLDREFLKNEIDNVRAQLSQDKRKRSQVIITDLRDLTEERN 60  
 :|||||  
 DB 56 RHIIISRLFDVGLDDSDDEPSLQNEIDRVKVNFFSSKERBWRQKAMDLMETVELQ 115  
 QY 61 ATVVSLOALGKAEMLGSLTKKOKKYLEQODETKQAQEEAGRLRSKKTMEQIELLQS 120  
 :|||||  
 DB 116 KALENLQDVMEKELCSLFTQMTYLESQNDPRAAEVYRRLRIKKTESLDVVLQ 175  
 QY 121 QLPVEEMIRDMGVGQSAVEQLAYCVSLKKEYENLKEARKAGEVADKLKDLFFSSRSK 180  
 :|||||  
 DB 176 QRAVESMITDMGIGQAAVEQLAYCVSLKKEYENLKEARKAGEVADKLKDLFFSSRSK 235  
 QY 181 LQTVYSELDAQKLELSAQKDLQSAKDEIKSLKKRLMLQ 220  
 :|||||  
 DB 236 LHKALLELTAKARDMKSQNDLDTNAKEIKSLKKVEFLQ 275

## RESULT 7

Q96062 PRELIMINARY; PRT; 1958 AA.

AC Q96062;  
 DT 01-MAY-1999 (TREMblrel. 10, Created)  
 DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)  
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
 DE MYOSIN HEAVY CHAIN.  
 GN DJMHC-A.  
 OS Dugesia japonica (Planarian).  
 OC Eukaryota; Metazoa; Platyhelminthes; Turbellaria; Seriata; Tricladida;  
 OC Paludicola; Dugesidae; Dugesia.  
 OX NCBI\_TaxID=6161;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kobayashi C., Kobayashi S., Oril H., Agata K., Watanabe K.;  
 RT "Identification of two distinct muscles in the planarian, Dugesia  
 RT japonica, by the expression of myosin heavy chain genes.";  
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AB015484; BAA34954.1; -.  
 DR HSSP; P24733; IMDC.  
 DR InterPro: IPR001064; Crystallin.







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Query Match      15.4%; Score 164; DB 5; Length 692;
Best Local Similarity 22.1%; Pred. No. 0.06;
Matches 65; Conservative 63; Mismatches 78; Indels 88; Gaps 11;

QY 4 INKLFPLA-----QEEENVLDREF--LNKNELDN---VRAQLSQ-----KDKRK 42
DB 104 INRVIELTSHKQRLSEENVLEIKVEHVKLQDNANHLKTLQALQOELEDRHRLFEERK 163
QY 43 RDS-----QYIIDLRLPTLEERNATVVSLOQALGKA-----73
DB 164 RASLENNHATLEVELESILKYLQDESEARLERLQTKRANGADASMKSEAYEALQAHDE 223
QY 74 -----ML-----CSTLKKOMKYLEQOD---EKKQOEAGRLRSK 107
DB 224 VEELRRMAOKISFEYEQALALNKKCSLEKQSRLOSEVYLIMLEKATRRHQLEKR 283
QY 108 MKTMEQIELLQSLPEVEEMIRDMGVGOSAVEQLAVYCVSLKK---EYENLKEARRASG 164
DB 284 VAQLEKINLIDKKNLEVTMLM-----EQAKELRYKINELQKLGHEYELRQROOLA 337
QY 165 EVADKLKRDYFSSRSKLTQTYVELDQAKLEK---SAQKDIQSADKEIMSLKKK 215
DB 338 RENMKITDDLAEAKSQLDNDAHRRIRHEQIEIKLENERDELSAAYKEAETLRKQ 391

RESULT 16
043241 PRELIMINARY; PRT; 1530 AA.
ID 043241;
AC 043241;
DT 01-JUN-1998 (TReMBLrel. 06, Created)
DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE GCP170.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97442456; Pubmed=9295333;
RA Msumi Y., Sohma M., Yano A., Fujiwara T., Ikehara Y.;
RT "Molecular Characterization of GCP170, a 170-kDa Protein Associated
RT with the Cytoplasmic Face of the Golgi Membrane."
RL J. Biol. Chem. 272:23851-23858(1997).
DR EMBL: D63997; BAA23661.1;
SQ SEQUENCE 1530 AA; 170268 MW; E3851F2ABFA1A533 CRC64;

Query Match      15.4%; Score 164; DB 4; Length 1530;
Best Local Similarity 25.0%; Pred. No. 0.13;
Matches 60; Conservative 46; Mismatches 96; Indels 38; Gaps 7;

QY 13 QEEENVLDREFLNKNELD-----NVRALSQDKKEDSDQYIIDLRLPTLEERNATVVS 66
DB 1132 REHNSILEFALAKREALVQLNQLQVAVLQKKEBEDROMKHLYVALQASLEKEKEKNSL 1191
QY 67 QQALGKAEMLCSTLKKOMKYLEQOQDETK-----QAOEAGRLRSKMTWE- 112
DB 1192 KEQVAAAKVEGNHRRFKASLELSEYKKEQLAKENHLYQKLAEDADQLQREGKHSQEI 1251
QY 113 -----QIEL-----LQSLPEVEEMIRDMGVGOSAVEQLAVYCVSLKKEYNLKEARRK 161
DB 1252 AQQFAELAEARAOQLQLOKOL---DEQLSKQPVGNQOEENLKEWEDOKEREIQSLKQOLD 1308
QY 162 ASGEVADKLKRDYFSSRSKLTQTYVELDQAKLEKSAOKDQASADKEIMSLKKTL-TMLQ 220
DB 1309 LTBQGG---KRELGLQQLLQNLVASELEMAQEDLSMTQKDFMLQAKYSELKNNMKITLQ 1365

RESULT 17
090337

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ID 090337 PRELIMINARY; PRT; 1933 AA.
AC 090337;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE MYOSIN HEAVY CHAIN.
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Cyprinus.
OX NCBI_TaxID=7962;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=FAST SKELETAL MUSCLE;
RX MEDLINE=97352533; Pubmed=9208928;
RA Hirayama Y., Matsuda S.;
RT "Structural differences in the crossbridge head of temperature-
RT associated myosin subfragment-1 isoforms from carp fast skeletal
RT muscle."
RL Eur. J. Biochem. 246:380-387(1997).
RN [2]
RP SEQUENCE OF 738-1933 FROM N.A.
RC TISSUE=FAST SKELETAL MUSCLE;
RX MEDLINE=97176447; Pubmed=9023993;
RA Inai J., Hirayama Y., Kikuchi K., Kakinuma M., Matsuda S.;
RT "cDNA cloning of myosin heavy chain isoforms from carp fast skeletal
RT muscle and their gene expression associated with temperature
RT acclimation."
RL J. Exp. Biol. 200:27-34(1997).
DR EMBL: D89990; BAA22067.1;
DR EMBL: D50474; BAA09067.1;
DR HSSP: P1338; 2MYS.
DR InterPro: IPR000048; IQ.
DR InterPro: IPR001609; myosin_head.
DR InterPro: IPR004009; Myosin_N.
DR InterPro: IPR002928; Myosin_tail.
DR Pfam: PF00612; IQ; 1.
DR Pfam: PF00663; myosin_head; 1.
DR Pfam: PF02736; Myosin_N; 1.
DR Pfam: PF01576; Myosin_Tail; 1.
DR PRINTS: PR00193; MYOSINHEAVY.
DR ProDom: PD000355; myosin_head; 1.
DR SMART: SM00015; IQ; 1.
DR SMART: SM00242; MYSC; 1.
DR PROSITE: PSS0096; IQ; 1.
KW Myosin.
SQ SEQUENCE 1933 AA; 221092 MW; CDF0CBA4475530F5 CRC64;

Query Match      15.3%; Score 163; DB 13; Length 1933;
Best Local Similarity 23.1%; Pred. No. 0.18;
Matches 59; Conservative 50; Mismatches 86; Indels 60; Gaps 8;

QY 15 EENVLDREF-----LNKNELDNVRALSQDKKEDSDQYIIDLRLPTLEER 59
DB 1178 EESTLGHATAALARKQADSVAEIGEDIDNLQRIKQLEKEKEKYEKNEIDDLSSNNE- 1235
QY 60 NATVVSLOQALGKAEMLCSTLKKOMKYLEQOQDETKQAOEAGRLRSKMT-----M 111
DB 1236 -----AVAKAGNLEKCKRTLEDQLSEIKAKSDENSROLNMMNQRARLQTEENSEFSROL 1290
QY 112 EQLLELQSLP-----EVEEMIRDMGVGOSAVEQLAVYCVSLKKEYNL 156
DB 1291 EKEKALV-SQLTRGKQAFQTQOIEDLKRHVEEVAKKNALAHAVOSARHDCDLQEEYEEE 1349
QY 157 KEAR-----KASGEVAD---RLRKDLFSSRSKLTQTYVELDQAKLEKSAOKDQSA 205
DB 1350 QEAKAEIQRGMSKNSVQAQRAKAYETDALTQRTBELSESKKKLQ---RLQDADESLAV 1406
QY 206 DKETMSLKKITLMLQ 220
DB 1407 NSKCSLEKTKORLQ 1421

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RESULT 23
Q9QYT3 PRELIMINARY: PRT: 1487 AA.
ID Q9QYT3
AC Q9QYT3:
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-OCT-2001 (Tremblrel. 18, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE MALE ENHANCED ANTIGEN 2/GOLGI AUTOANTIGEN, GOLGIN SUBFAMILY A, 3.
GN MEA2/GOLGA3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL6;
RA Matsukuma S.;
RT "Mea2/Golga3 Gene Product is indispensable for Spermatogenesis in the
RT Mouse."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB029537; BAA66889.2; -.
DR EMBL: AB029521; BAA66889.2; JOINED.
DR EMBL: AB029522; BAA66889.2; JOINED.
DR EMBL: AB029523; BAA66889.2; JOINED.
DR EMBL: AB029524; BAA66889.2; JOINED.
DR EMBL: AB029525; BAA66889.2; JOINED.
DR EMBL: AB029526; BAA66889.2; JOINED.
DR EMBL: AB029527; BAA66889.2; JOINED.
DR EMBL: AB029528; BAA66889.2; JOINED.
DR EMBL: AB029529; BAA66889.2; JOINED.
DR EMBL: AB029530; BAA66889.2; JOINED.
DR EMBL: AB029531; BAA66889.2; JOINED.
DR EMBL: AB029532; BAA66889.2; JOINED.
DR EMBL: AB029533; BAA66889.2; JOINED.
DR EMBL: AB029534; BAA66889.2; JOINED.
DR EMBL: AB029535; BAA66889.2; JOINED.
DR EMBL: AB029536; BAA66889.2; JOINED.
SQ SEQUENCE 1487 AA; 167175 MW; 5BADF716C251EBFF CRC64;

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Query Match 15.1%; Score 161; DB 11; Length 1487;
Best Local Similarity 23.1%; Pred. No. 0.18;
Matches 57; Conservative 48; Mismatches 90; Indels 52; Gaps 7;

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QY 13 QEEVNLDFREFLNELD-----NVRAQLSQKREKRDPOVIIDTLRDLTEERNATVSL 66
ID Q9NM23 PRELIMINARY: PRT: 1219 AA.
AC Q9NM23:
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE MYOSIN HEAVY CHAIN STRIATED MUSCLE SPECIFIC ISOFORM (FRAGMENT).
GN MHC.
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Pectinoida;
OC Pectinoidae; Pectinidae; Argopecten.
OX NCBI_TaxID=31199;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=20090924; PubMed=10623517;
RA Yamada A., Yoshio M., Owa K., Nyitray L.;
RT "Catchin, a novel protein in mollusc catch muscles, is produced by
RT alternative splicing from the myosin heavy chain gene."
RL J. Mol. Biol. 295:169-178(2000).
DR EMBL: AF183909; AAF62391.1; -.
DR HSSP; P24733; IMDC.
DR InterPro; IPR000048; IQ.
DR InterPro; IPR001609; myosin_head.
DR InterPro; IPR002928; myosin_tail.
DR InterPro; IPR002017; Spectrin.
DR InterPro; IPR000533; Tropomyosin.
DR Pfam; PF00612; IQ; 2.
DR Pfam; PF00063; myosin_head; 1.
DR Pfam; PF01576; myosin_tail; 1.

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```

RESULT 24
Q9BMM8 PRELIMINARY: PRT: 876 AA.
ID Q9BMM8
AC Q9BMM8:
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE PARAMYOSIN.

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OS Sarcophes scabiei.
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Acariformes; Sarcopififormes; Astigmata; Sarcopifidae; Sarcopifidae;
OC Sarcophes.
OX NCBI_TaxID=52283;
RN [1]
RP SEQUENCE FROM N.A.
RA Mattsson J.G., Ljunggren E.L., Bergstrom K.;
RT "Paramyosin from the parasitic mite Sarcophes scabiei: cDNA cloning
RT and heterologous expression."
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF317670; AAK0181.1; -.
DR InterPro; IPR002928; Myosin_tail.
DR InterPro; IPR001854; Ribosomal_L29.
DR Pfam; PF01576; Myosin_tail; 1.
SQ SEQUENCE 876 AA; 102454 MW; C99475EE7A0DAE52 CRC64;

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Query Match 15.1%; Score 160.5; DB 5; Length 876;
Best Local Similarity 24.6%; Pred. No. 0.12;
Matches 64; Conservative 49; Mismatches 90; Indels 57; Gaps 9;

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```

QY 5 NKLFPDLQOE-----EENVLDREFLN-----ELDNVRAQL----- 35
ID Q9NM23 PRELIMINARY: PRT: 1219 AA.
AC Q9NM23:
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE MYOSIN HEAVY CHAIN STRIATED MUSCLE SPECIFIC ISOFORM (FRAGMENT).
GN MHC.
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Pectinoida;
OC Pectinoidae; Pectinidae; Argopecten.
OX NCBI_TaxID=31199;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=20090924; PubMed=10623517;
RA Yamada A., Yoshio M., Owa K., Nyitray L.;
RT "Catchin, a novel protein in mollusc catch muscles, is produced by
RT alternative splicing from the myosin heavy chain gene."
RL J. Mol. Biol. 295:169-178(2000).
DR EMBL: AF183909; AAF62391.1; -.
DR HSSP; P24733; IMDC.
DR InterPro; IPR000048; IQ.
DR InterPro; IPR001609; myosin_head.
DR InterPro; IPR002928; myosin_tail.
DR InterPro; IPR002017; Spectrin.
DR InterPro; IPR000533; Tropomyosin.
DR Pfam; PF00612; IQ; 2.
DR Pfam; PF00063; myosin_head; 1.
DR Pfam; PF01576; myosin_tail; 1.

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```

RESULT 25
Q9NM23 PRELIMINARY: PRT: 1219 AA.
ID Q9NM23
AC Q9NM23:
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE MYOSIN HEAVY CHAIN STRIATED MUSCLE SPECIFIC ISOFORM (FRAGMENT).
GN MHC.
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Pectinoida;
OC Pectinoidae; Pectinidae; Argopecten.
OX NCBI_TaxID=31199;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=20090924; PubMed=10623517;
RA Yamada A., Yoshio M., Owa K., Nyitray L.;
RT "Catchin, a novel protein in mollusc catch muscles, is produced by
RT alternative splicing from the myosin heavy chain gene."
RL J. Mol. Biol. 295:169-178(2000).
DR EMBL: AF183909; AAF62391.1; -.
DR HSSP; P24733; IMDC.
DR InterPro; IPR000048; IQ.
DR InterPro; IPR001609; myosin_head.
DR InterPro; IPR002928; myosin_tail.
DR InterPro; IPR002017; Spectrin.
DR InterPro; IPR000533; Tropomyosin.
DR Pfam; PF00612; IQ; 2.
DR Pfam; PF00063; myosin_head; 1.
DR Pfam; PF01576; myosin_tail; 1.

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RA Yamada A., Yoshio M., Olwa K., Nyitray L.;  
RT "Catchin, a novel protein in molluscan catch muscles, is produced by  
RT alternative splicing from the myosin heavy chain gene.";  
RL J. Mol. Biol. 295:169-178(2000).  
DR EMBL: AF183909; AAF62392.1; -.  
DR HSSP: P24733; IMDC.  
DR InterPro: IPR000048; IQ.  
DR InterPro: IPR001609; myosin\_head.  
DR InterPro: IPR002928; Myosin\_tail.  
DR InterPro: IPR002017; Spectrin.  
DR InterPro: IPR000533; Tropomyosin.  
DR Pfam: PF00063; myosin\_head; 1.  
DR Pfam: PF01576; Myosin\_tail; 1.  
DR PRINTS: PR00194; TROPOMYOSIN.  
DR ProDom: PD000355; myosin\_head; 1.  
DR SMART: SM00015; IQ; 1.  
DR PROSITE: PS50096; IQ; 1.  
DR NON\_TER 1  
FT SEQUENCE 1229 AA; 142180 MW; 1764276CB904FDC9 CRC64;  
SQ

Query Match 15.0%; Score 159.5; DB 5; Length 1229;  
Best Local Similarity 27.4%; Pred. No. 0.19; Mismatches 75; Indels 27; Gaps 7;  
Matches 57; Conservative 49;

QY 10 DLAGEENVLDREFLNKL-DNVR--AQLSQDKERKDSQYIIDTLRDLTEERNATVVS 65  
DB 336 DLKSTQENVDELRVKRELEENVRRKEAISLSNKLDEQNLVSQLOKRIKELQARIEE 395  
QY 66 LQALGKAEMLCSTLKQMKYLEQOODETKQAQEEAGRLRSKMKMTMEQIELLSQLPVEV 125  
DB 336 LEEELAEARNARAKVEKQRAELRELELGERLDEAGC----ATSAQELNKKRE-AEL 449  
QY 126 EEMIDMGVGSABVQLAVVYCVSLKKEYENLKEARKASGEVADKLKDLFSSRSKLQTVY 185  
DB 450 LKIRRDLD--EASLQHEAQISALRKHOD-----AANEMADQV-----DQLQKVK 492  
QY 186 SELDQAKLELKSQKDLQSDAKETMSLK 213  
DB 493 SKSEKQKQQLRSEVEDLQAQIOHISKNK 520

RESULT 29  
Q9NJ21 PRELIMINARY; PRT; 1243 AA.  
AC Q9NJ21;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE MYOSIN HEAVY CHAIN CARDIAC MUSCLE SPECIFIC ISOFORM 1 (FRAGMENT).  
GN MHC.  
OS Aequiptecten irradians (Bay scallop).  
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Pectinoidea;  
OC Pectinoidea; Pectinidae; Argopecten.  
OX NCBI\_TaxID=31199;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20090924; PubMed=10623517;  
RA Yamada A., Yoshio M., Olwa K., Nyitray L.;  
RT "Catchin, a novel protein in molluscan catch muscles, is produced by  
RT alternative splicing from the myosin heavy chain gene.";  
RL J. Mol. Biol. 295:169-178(2000).  
DR EMBL: AF183909; AAF62394.1; -.  
DR HSSP: P24733; IMDC.  
DR InterPro: IPR000048; IQ.  
DR InterPro: IPR001609; myosin\_head.  
DR InterPro: IPR002928; Myosin\_tail.  
DR InterPro: IPR002017; Spectrin.  
DR InterPro: IPR000533; Tropomyosin.  
DR Pfam: PF00063; myosin\_head; 1.  
DR Pfam: PF01576; Myosin\_tail; 1.  
DR PRINTS: PR00194; TROPOMYOSIN.  
DR ProDom: PD000355; myosin\_head; 1.

DR SMART: SM00015; IQ; 1.  
DR PROSITE: PS50096; IQ; 1.  
FT NON\_TER 1  
SQ SEQUENCE 1243 AA; 143531 MW; B5C7219BF2B8AE CRC64;

Query Match 15.0%; Score 159.5; DB 5; Length 1243;  
Best Local Similarity 27.4%; Pred. No. 0.19; Mismatches 75; Indels 27; Gaps 7;  
Matches 57; Conservative 49;

QY 10 DLAGEENVLDREFLNKL-DNVR--AQLSQDKERKDSQYIIDTLRDLTEERNATVVS 65  
DB 336 DLKSTQENVDELRVKRELEENVRRKEAISLSNKLDEQNLVSQLOKRIKELQARIEE 395  
QY 66 LQALGKAEMLCSTLKQMKYLEQOODETKQAQEEAGRLRSKMKMTMEQIELLSQLPVEV 125  
DB 336 LEEELAEARNARAKVEKQRAELRELELGERLDEAGC----ATSAQELNKKRE-AEL 449  
QY 126 EEMIDMGVGSABVQLAVVYCVSLKKEYENLKEARKASGEVADKLKDLFSSRSKLQTVY 185  
DB 450 LKIRRDLD--EASLQHEAQISALRKHOD-----AANEMADQV-----DQLQKVK 492  
QY 186 SELDQAKLELKSQKDLQSDAKETMSLK 213  
DB 493 SKSEKQKQQLRSEVEDLQAQIOHISKNK 520

RESULT 30  
Q9NJ20 PRELIMINARY; PRT; 1253 AA.  
AC Q9NJ20;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE MYOSIN HEAVY CHAIN CARDIAC MUSCLE SPECIFIC ISOFORM 2 (FRAGMENT).  
GN MHC.  
OS Aequiptecten irradians (Bay scallop).  
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Pectinoidea;  
OC Pectinoidea; Pectinidae; Argopecten.  
OX NCBI\_TaxID=31199;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20090924; PubMed=10623517;  
RA Yamada A., Yoshio M., Olwa K., Nyitray L.;  
RT "Catchin, a novel protein in molluscan catch muscles, is produced by  
RT alternative splicing from the myosin heavy chain gene.";  
RL J. Mol. Biol. 295:169-178(2000).  
DR EMBL: AF183909; AAF62395.1; -.  
DR HSSP: P24733; IMDC.  
DR InterPro: IPR000048; IQ.  
DR InterPro: IPR001609; myosin\_head.  
DR InterPro: IPR002928; Myosin\_tail.  
DR InterPro: IPR002017; Spectrin.  
DR InterPro: IPR000533; Tropomyosin.  
DR Pfam: PF00063; myosin\_head; 1.  
DR Pfam: PF01576; Myosin\_tail; 1.  
DR PRINTS: PR00194; TROPOMYOSIN.  
DR ProDom: PD000355; myosin\_head; 1.  
DR SMART: SM00015; IQ; 1.  
DR PROSITE: PS50096; IQ; 1.  
FT NON\_TER 1  
SQ SEQUENCE 1253 AA; 144774 MW; 56E4FF0226B58C92 CRC64;

Query Match 15.0%; Score 159.5; DB 5; Length 1253;  
Best Local Similarity 27.4%; Pred. No. 0.19; Mismatches 75; Indels 27; Gaps 7;  
Matches 57; Conservative 49;

QY 10 DLAGEENVLDREFLNKL-DNVR--AQLSQDKERKDSQYIIDTLRDLTEERNATVVS 65  
DB 336 DLKSTQENVDELRVKRELEENVRRKEAISLSNKLDEQNLVSQLOKRIKELQARIEE 395  
QY 66 LQALGKAEMLCSTLKQMKYLEQOODETKQAQEEAGRLRSKMKMTMEQIELLSQLPVEV 125

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Db 396 LEELEAEARNARAKVEKQRAELNRELEBELGRLEDEAGG-----ATSAQIELNKKRE-AEL 449
Qy 126 EEMIRDMGVGQSAVEQOLAVYCVSLKKEVENLKEARKASGEVADLRDLFSSRSKLQTVY 185
Db 450 LKIRRD-EEASLQHEAQAISALRKKHOD-----AANEMADQV-----DQLQKVK 492
Qy 186 SELDOAKLELKSAAQKDLQSADEKIMSUK 213
Db 493 SKSEKEKQQLRSEVEDLQAOIQIHISKNK 520

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RESULT 31
Q17042 PRELIMINARY; PRT; 1951 AA.
ID 017042
AC 017042;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE MYOSIN HEAVY CHAIN.
OS Aequipecten irradians (Bay scallop).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Pectinoidea;
OC Pectinoidea; Pectinidae; Argopecten.
OX NCBI_TaxID=31199;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MUSCLE, CATCH (SMOOTH) ADDUCTOR;
RX MEDLINE=95108023; Pubmed=7809102;
RA Nyltday L., Janoso A., Ochial Y., Graf L., Szent-Gyorgyi A.G.;
RT "Scallop striated and smooth muscle myosin heavy-chain isoforms are
RT produced by alternative RNA splicing from a single gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:12686-12690(1994).
DR EMBL: U09782; AAC46490.1; -
DR HSSP: P24733; 1MDC.
DR InterPro: IPR000048; IQ.
DR InterPro: IPR001609; myosin_head.
DR InterPro: IPR004009; Myosin_N.
DR InterPro: IPR002928; Myosin_tail.
DR InterPro: IPR002017; Spectrin.
DR Pfam: PR00612; IQ_2.
DR Pfam: PF00063; myosin_head; 1.
DR Pfam: PF02736; Myosin_N; 1.
DR Pfam: PF01576; Myosin_tail; 1.
DR PRINTS: PR00193; MYOSINHEAVY.
DR PRODOM: PD000355; myosin_head; 1.
DR SMART: SM00015; IQ_1.
DR SMART: SM00242; MYSC; 1.
DR PROSITE: PS50096; IQ; 1.
SQ SEQUENCE 1951 AA; 224253 MW; 1FDC3D7D691C1410 CRC64;

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Query Match 15.0%; Score 159.5; DB 5; Length 1951;
Best Local Similarity 27.4%; Pred. No. 0.29;
Matches 57; Conservative 49; Mismatches 75; Indels 27; Gaps 7;

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```

Qy 10 DLAGEENVLDREFLKNEL-DNVR---AQLSOKDEKRDQSVIITDITLDTLEARNATVVS 65
Db 1058 DLKSTQENVLELRYKKLEENVRKREKAEISLSKLEDEBQNLVSQLRKTKELQARIEE 1117
Qy 66 LQALGKAEMLCSTLKKOMKYLEOQOODETKQAQOEAGRLRSKMTMEQIELLLOSQLEPV 125
Db 1118 LEELEAEARNARAKVEKQRAELNRELEBELGRLEDEAGG-----ATSAQIELNKKRE-AEL 1171
Qy 126 EEMIRDMGVGQSAVEQOLAVYCVSLKKEVENLKEARKASGEVADLRDLFSSRSKLQTVY 185
Db 1172 LKIRRD-EEASLQHEAQAISALRKKHOD-----AANEMADQV-----DQLQKVK 1214
Qy 186 SELDOAKLELKSAAQKDLQSADEKIMSUK 213
Db 1215 SKSEKEKQQLRSEVEDLQAOIQIHISKNK 1242

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RESULT 32

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Q07569
ID 007569 PRELIMINARY; PRT; 2139 AA.
AC 007569; 002504;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE MYOSIN HEAVY CHAIN.
GN MHCA.
OS Entamoeba histolytica.
OC Eukaryota; Entamoebidae; Entamoeba.
OX NCBI_Taxid=5759;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HMI:IMSS;
RX MEDLINE=93295430; Pubmed=8515774;
RA Raymond-Denise A., Sansonetti P., Guillen N.;
RT "Identification and characterization of a myosin heavy chain gene
RT (mhca) from the human parasitic pathogen Entamoeba histolytica.";
RL Mol. Biochem. Parasitol. 59:123-131(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=HMI:IMSS;
RA Guillen N.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: L03534; AAB48065.1; -
DR HSSP: P08799; 1MND.
DR InterPro: IPR000048; IQ.
DR InterPro: IPR001609; myosin_head.
DR Pfam: PF00612; IQ_2.
DR Pfam: PF00063; myosin_head; 1.
DR PRINTS: PR00193; MYOSINHEAVY.
DR PRODOM: PD000355; myosin_head; 1.
DR SMART: SM00242; MYSC; 1.
SQ SEQUENCE 2139 AA; 245225 MW; C68307341DB51DD1 CRC64;

```

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Query Match 15.0%; Score 159.5; DB 5; Length 2139;
Best Local Similarity 24.0%; Pred. No. 0.33;
Matches 60; Conservative 49; Mismatches 96; Indels 45; Gaps 7;

```

```

Qy 5 NKLFFDL--AOEENVLDREFLKNELDNVRAQLSOKDEKRDQSVI-----ID 50
Db 1144 NKIEGDLRNAQRIKIKELDEITKGA--DV-SQYLQKQKEEYESQLAKMQEKEAIGNDVK 1200
Qy 51 TLRLTLEARNATVVSLSQALGKAEMLCSTLKKOMKYLEOQOODETKQAQOEAGRLRSKMT 110
Db 1201 NKEKTIKKELEISLQRLDETEVEKEDAKRKKKEIK---EMKALQDEKEWESSKNS 1257
Qy 111 MEQIEELLQSOLPEVEEMIRDMGVGQSAVEQOLAVYCVSLKKEVENLKEARKASGEVADKL 170
Db 1258 TEKDKKKLELDNIKTQKKLDMWTADNEKLUKAKAKLEQNLNEVDNHEKAVADAELNKK 1317
Qy 171 R---KDLFSSRSKLQ-----TVSELDQAKLELKSAAQKDLQSA 205
Db 1318 KAQSDKELNSLKALELALTKAKSVESKNKDSENEKALSEIDQANKEKLNIQADLRKA 1377
Qy 206 DKEIMSLKK 215
Db 1378 TADLQEANER 1387

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RESULT 33
Q07380 PRELIMINARY; PRT; 1790 AA.
ID 007380
AC 007380; P89892;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE HYPOTHETICAL 206.5 KDA PROTEIN YDL058W.
GN USO1 OR YDL058W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.

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OX NCBI\_TaxID=4932;  
 RN [1]  
 RA SEQUENCE FROM N.A.  
 RL Bloeker H., Brandt P.;  
 Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; 274106; CA98621.1; -  
 DR EMBL; 274105; CA98620.1; -  
 DR SGD; S0002216; USOL.  
 DR InterPro: IPR002017; Spectrin.  
 SO SEQUENCE 1790 AA; 206450 MW; 90062544F55A52EE CRC64;

Query Match 14.9%; Score 159; DB 3; Length 1790;  
 Best Local Similarity 23.7%; Pred. No. 0.29;  
 Matches 61; Conservative 57; Mismatches 85; Indels 54; Gaps 9;

OY 1 RTITKLEFPDLAQ---EEENVLDREFLK-----NELDNVRAQLSOKDKKRDQOVI 48  
 Db 1369 RRLNEGSSITIOEYSEKINTELEDIRLQENENELKAEIDMTRESEL-EKVSLSMD---- 1423  
 OY 49 IDTLDTLEERNATVVSLOQAL-----GKAEMLCSTLKKQMKYLBQODETKQAQEE 100  
 Db 1424 -----ELLEKONTIKSLQDELSTKDKITRNDKLTSTERNKRDLESLEKQLRAQDS 1478  
 OY 101 AGRLSKMKTMEOILQLQOLPEVEEMIRDMGVGQSAVE---QLAVYCVSLKKEYEVL 156  
 Db 1479 KAKVEGLKLTLEESSEKAELEKSEMMKKL---ESTIESMETLKSSMETIRKSDKL 1535  
 OY 157 KEARKASEVADKLR-----KDLFSSRSKIQTVY---SELDQAKLELKSQ 199  
 Db 1536 EOSKRSASEEDIKNLQHEKSDLSIRINESEKIDIEELSKLRLEPAKSGSELETYKQELNNAQ 1595  
 OY 200 KDLOSADKEIMSLKKKL 216  
 Db 1596 EKIRINAEENTVYLSKL 1612

RESULT 34  
 O9TV61 PRELIMINARY; PRT: 1939 AA.  
 AC O9TV61;  
 DT 01-MAY-2000 (TREMblrel. 13, Created)  
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
 DE MYOSIN HEAVY CHAIN 2X.  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=LANDRACE; TISSUE=SKLETAL MUSCLE;  
 RA Chikuni K., Tanabe R., Muroya S., Nakajima I.;  
 RT "Differences in molecular structure among the porcine myosin heavy  
 chain-2a, -2x, and -2b isoforms.";  
 RL Meat Sci. 57:311-317(2001).  
 DR EMBL; AB025262; BAA82146.1; -  
 DR HSSP; P13538; 2MYS.  
 DR InterPro: IPR000048; IQ.  
 DR InterPro: IPR001609; myosin\_head.  
 DR InterPro: IPR004009; myosin\_N.  
 DR InterPro: IPR002928; Myosin\_tail.  
 DR Pfam; PF00612; IQ; 2.  
 DR Pfam; PF00063; myosin\_head; 1.  
 DR Pfam; PF02736; myosin\_N; 1.  
 DR Pfam; PF01576; myosin\_tail; 1.  
 DR PRINTS; PR00193; MYOSINHEAVY.  
 DR ProDom; PD000355; myosin\_head; 1.  
 DR SMART; SM00015; IQ; 1.  
 DR SMART; SM00242; MYSC; 1.  
 DR PROSITE; PSS0096; IQ; 1.  
 SO SEQUENCE 1939 AA; 223172 MW; B702ADB599602ECB CRC64;

Query Match 14.9%; Score 159; DB 6; Length 1939;  
 Best Local Similarity 24.2%; Pred. No. 0.31;  
 Matches 55; Conservative 48; Mismatches 80; Indels 44; Gaps 7;

OY 24 LKNELDNVRAQLSOKDKERDSQVIITDLRTLEERNATVVSLOQALGKAEMLCSTLKKQ 83  
 Db 1207 LGEQIDNLQRYQVKLEKESEKMEIDLASNME-----TVSKAKGLKMKCTLEDO 1259  
 OY 84 MKYLEQODETK-----QAOEEAGRL-----RSKMKTMEOIELL 117  
 Db 1260 LSELKTEEEQORLINDLTAORARLQTESGEYSRQJDEKDTLVLSKQKQAFQOIEEL 1319  
 OY 118 LOSQPEVEEMIRDMGVGQSAVEQLAVYCVSLKKEYEMLKEARKASGEVADLRKDFSS 177  
 Db 1320 KR-----QLEEEIKAKSALAHAVQSSRHQCDLREQYEEEOEKAKELQRAMSKANSEVQW 1375  
 OY 178 RSKIQT---VYSELDQAKLELKSQKDLQSDAKKEIMSLKKLTMLQ 220  
 Db 1376 RTKYETDAIORTLEELKAEKKL--AQR--LQDAEEHVAVMKCASTLE 1419

RESULT 35  
 Q26079 PRELIMINARY; PRT: 1941 AA.  
 ID Q26079;  
 AC Q26079;  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
 DE MYOSIN HEAVY CHAIN.  
 OS Placocysten magellanicus (Sea scallop).  
 CC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Pectinoida;  
 OC Pectinoidea; Pectinidae; Placopecten.  
 NCBI\_TaxID=6577;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=SKLETAL MUSCLE;  
 RA Perreault-Micale C., Kalabokis V., Nyitrai L., Szent-Gyorgyi A.G.;  
 RT "Sequence variations in the surface loop near the nucleotide binding  
 site modulate the ATP turnover rates of molluscan myosins.";  
 RL J. Muscle Res. Cell Motil. 0:0-0(1996).  
 DR EMBL; U59294; AAB03660.1; -  
 DR HSSP; P24733; IMDC.  
 DR InterPro: IPR000048; IQ.  
 DR InterPro: IPR001609; myosin\_head.  
 DR InterPro: IPR004009; myosin\_N.  
 DR InterPro: IPR002928; Myosin\_tail.  
 DR InterPro: IPR002017; Spectrin.  
 DR Pfam; PF00612; IQ; 2.  
 DR Pfam; PF00063; myosin\_head; 1.  
 DR Pfam; PF02736; myosin\_N; 1.  
 DR Pfam; PF01576; myosin\_tail; 1.  
 DR PRINTS; PR00193; MYOSINHEAVY.  
 DR ProDom; PD000355; myosin\_head; 1.  
 DR SMART; SM00015; IQ; 1.  
 DR SMART; SM00242; MYSC; 1.  
 DR PROSITE; PSS0096; IQ; 1.  
 SO SEQUENCE 1941 AA; 223243 MW; E2AD1637FFDB8127 CRC64;

Query Match 14.9%; Score 158.5; DB 5; Length 1941;  
 Best Local Similarity 27.5%; Pred. No. 0.33;  
 Matches 56; Conservative 49; Mismatches 72; Indels 27; Gaps 7;  
 OY 5 NKLFFDLAQEEENVLDREFLKNEI-DNVR---AQLSOKDKERDSQVIITDLRTLEERN 60  
 Db 1053 SKVEDLKTSDQENVEDLERVARELEENVRKREAEITTLNSKLEDEQNIVSOLQRIKELQ 1112  
 OY 61 ATVVSLOQALGKAEMLCSTLKKQMKYLBQODETKQAQEEAGRLSKMKTMEOIELLQS 120  
 Db 1113 ARIELEELLEARNARKSVKQRELRLELEEGERLDEAGG---ATSAQILELNKRK 1167  
 OY 121 QLPEVEEMIRDMGVGQSAVEQLAVYCVSLKKEYEMLKEARKASGEVADKLKDLFSSRSK 180

Db 1168 E-ABLTKIRRLD---EESASLOHEAHOISAIRKHOD-----AAENEMADQV-----DQ 1209  
 QY 181 LQTVYSELDOAKLELKSADKLDOS 204  
 Db 1210 LQVKSKLEKDKDKLREMDLES 1233

RESULT 36  
 Q91520 PRELIMINARY; PRT: 786 AA.

AC Q91520; 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
 DE SKELETAL MYOSIN HEAVY CHAIN (FRAGMENT).  
 OS Thunnus thynnus (Bluefin tuna).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Perciformes; Scombroidei;  
 OC Scombridae; Thunnus.  
 NC NCBL\_Taxid=8237;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=FAST MUSCLE;  
 RA Hirayama Y., Watabe S.;  
 RT "cDNA cloning of bluefin tuna skeletal muscle myosin heavy chain.";  
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: D8138; BAA1730.1; -;  
 DR InterPro: IPR002928; Myosin\_tail.  
 DR InterPro: IPR000533; Tropomyosin.  
 DR Pfam: PF01576; Myosin\_tail; 1.  
 DR PRINTS: PR00194; TROPOMYOSIN.  
 FT NON\_TER 1  
 SQ SEQUENCE 786 AA; 90580 MW; 0279F714CA649A10 CRC64;

Query Match 14.7%; Score 156.5; DB 13; Length 786;  
 Best Local Similarity 24.0%; Pred. No. 0.18;  
 Matches 63; Conservative 48; Mismatches 91; Indels 61; Gaps 9;

QY 6 KLFDLAEENVDREF-----LKNELDNVRAQLSOKDKERKSOVIID 50  
 Db 23 KLRLD---EESTLQHEATSASLRKQADVAELEQIDNLRVQKLEKESYKMEID 79  
 QY 51 TLRLTLEERNATVSLQALGKAEMLCSTLKQKYLEQODETRKQAOEEGRLSKMT 110  
 Db 80 DLSSNME-----AVAKSKGNLEKMCRTIEDQLSELKAKNDEHYRLNDLNGQRLQRT 132  
 QY 111 -----MEQIEL--LLOSQLP-----EVEEMIRDMGVGSAVEQLAVYCVS 148  
 Db 133 ENGFSROIEKDALVSOQLTRGQATYQOIELKRHIEELKAKNALAHVQSAHRDCL 192  
 QY 149 LKKEYENLKEAR-----NAGEVAD--KLRRDLFSSRSKLTQTVYSELDOAKLELS 197  
 Db 193 LREQYEEQEKAGELQKMSKANSEVAQWRTYETDAIQRTPELEPAKKLAQ---RLQD 249  
 QY 198 AQKDLQSHDKETMSLKKTLMQ 220  
 Db 250 AESIEAVNSKASLEKTKRQLQ 272

RESULT 37  
 Q22276 PRELIMINARY; PRT: 1138 AA.  
 AC Q22276; 022294;  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)  
 DT 01-MAY-2000 (TREMblrel. 13, Last annotation update)  
 DE T07C4.10 PROTEIN.  
 GN T07C4.10.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;

OC Rhabditidae; Peloderinae; Caenorhabditis.  
 OX NCBL\_Taxid=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Buck D., Berks M.;  
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: 248055; CAA88136.1; -;  
 DR EMBL: 229443; CAA88136.1; JOINED.  
 DR EMBL: 229443; CAA82580.1; -;  
 DR EMBL: 248055; CAA82580.1; JOINED.  
 SQ SEQUENCE 1138 AA; 132785 MW; DF16C5F5A1B1155E CRC64;

Query Match 14.7%; Score 156.5; DB 5; Length 1138;  
 Best Local Similarity 24.7%; Pred. No. 0.25;  
 Matches 58; Conservative 45; Mismatches 73; Indels 59; Gaps 9;

QY 1 RTIINKLFFDLAEENVDREF--LKNELDNVRAQL-----SOKDEKR 43  
 Db 544 KTIYKENVY--LSESKQVLESEINLKNELDDEMAVKLRNSQHVAGLNEKISEEKRRRKQ 602  
 QY 44 DSOYIITLRLTLEERNATVVSLOALGKAEML--CSTLKQKYLEEQODETRKQOEBA 101  
 Db 603 DADV-----TRIDEQNKLT--LREADSSELLLEVQKGRKREIDHLRQQLAHOSSEAGSV 654  
 QY 102 GLRKSMTMEQIELLOSQLPVEEEMIRDMGVGSAVEQLAVYCVSLKKEYENLKEARK 161  
 Db 655 GQLQCKLAESHRRYLLQLLEFRYMKMERD-----LDGRIEYITSEA 697  
 QY 162 ASGEVADKLRRDLFSSRSKLTQTVYSELDOAKLELSAQKDLQSDAKETMSLKRL 216  
 Db 698 AANLELRLRKDTAEQKEKLEA-----MEWEARSKDLELAD-----LTRKL 738

RESULT 38  
 Q907E3 PRELIMINARY; PRT: 1940 AA.

AC Q907E3; 01-MAY-2000 (TREMblrel. 13, Created)  
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
 DE MYOSIN HEAVY CHAIN.  
 OS Pecten maximus (King scallop) (P1grim's clam).  
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Periomorpha; Pectinoida;  
 OC Pectinoida; Pectinidae; Pecten.  
 OX NCBL\_Taxid=6579;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=ADDUCTOR MUSCLE;  
 RA James D.P., Patel H., Chantler P.D.;  
 RT "Primary structure of myosin from the striated adductor muscle of the Atlantic scallop, Pecten maximus.";  
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF134172; AAD52842.1; -;  
 DR HSP: P24733; IWDG.  
 DR InterPro: IPR000048; IO.  
 DR InterPro: IPR001609; myosin\_head.  
 DR InterPro: IPR004009; myosin\_N.  
 DR InterPro: IPR002928; myosin\_tail.  
 DR InterPro: IPR002017; Spectrin.  
 DR Pfam: PF00612; IO; 2.  
 DR Pfam: PF00063; myosin\_head; 1.  
 DR Pfam: PF02736; myosin\_N; 1.  
 DR Pfam: PF01576; Myosin\_tail; 1.  
 DR PRINTS: PR00193; MYOSINHEAVY.  
 DR ProDom: PD000355; myosin\_head; 1.  
 DR SMART: SM00015; IO; 1.  
 DR SMART: SM00242; MYSC; 1.  
 DR PROSITE: PSS0096; IO; 1.  
 SQ SEQUENCE 1940 AA; 223141 MW; A3D09DECBEB16F90 CRC64;

Query Match 14.7%; Score 156.5; DB 5; Length 1940;

Best Local Similarity 27.6%; Pred. No. 0.43;  
Matches 55; Conservative 47; Mismatches 70; Indels 27; Gaps 7;

OY 10 DLAGEENVLDREFLNEL-DNVR---AQLSOKDKERDSQYIIDTLRDTLEERNATVS 65  
DB 1058 DAKSTQENVDEYKRELEENVRKREKSTLNKSLDEQNLVSQLRKYVELQARIEE 1117  
OY 66 LQALGKAKMLCSTLKKOMKYLEQOODETKQAQEAAGRLSRKMKTMEOIELLOSQLEPV 125  
DB 1118 LEEELAEARNNAKAYEKQRAELNRELDELGERLDEAG-----ATSAQIELNKKRE-AEL 1171  
OY 126 EEMIDMGVGSAYQQLAVYCVSLKKEYENLKAARKASGEVADKLKDLFSSRSKLQTVY 185  
DB 1172 LKIRIDL---EASLQHEAQSIALRKKHOD-----AANEMADQY-----DOLQRYK 1214  
OY 186 SELDAQLELKSQDKLOS 204  
DB 1215 SKLEKDKKDKREMDLES 1233

RESULT 39

OY 091ME7 PRELIMINARY; PRT; 959 AA.  
AC 091ME7;  
DT 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE SIMILAR TO TRANSYCOTOSIS ASSOCIATED PROTEIN.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=EYE, AND RETINA;  
RA Strausberg R.;  
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC016069; AAH16069.1;  
SQ SEQUENCE 959 AA; 106983 MW; 2C05DC35E899D81C CRC64;

Query Match 14.6%; Score 155.5; DB 11; Length 959;  
Best Local Similarity 19.5%; Pred. No. 0.25;  
Matches 64; Conservative 52; Mismatches 81; Indels 131; Gaps 8;

OY 15 EENVLDREFLK--NELDNV--RAQLSOKDKERDSQYIIDTLRDTLEERNATVS LQAL 70  
DB 605 EYMFIDHEFTLVKLEGVITKAIKSSSEDDKKEEV-----KTLLEQHDNIVTHYKMT 659  
OY 71 GKAEMLCSTLKKOMKYLEQODE---TKQAQ----- 98  
DB 660 REQDLQLEELKQOYSTLKCQNBQLOTAVTQASQIQOHKDDYNLLKVLGKDNHQSNG 719  
OY 99 -----EAGRLSRKMKTMEOIELLOSQLEPEVEMIRDMGVGSA--VEQLAVYC 146  
DB 720 DGAQVNGIQPEISRLREIEIELKSQALLOGLAELKDSLLENLKSQASGMSSEQASATC 779  
OY 147 ----- 146  
DB 780 PPRDPEOVAELKQELTALKSOLCSOSLEITRLQTECNELLQRAETLAKSVPEGESEHVS 839  
OY 147 -----VSLKKEYENLKAARKASGEVADKLKDLFSSRSKLQTVYSELDAQLEL 195  
DB 840 AAKTTDVEGRSLALLQETKELKNEKALSEERTAIQKQDSSNSTIATLQTEKDKLDLEV 899  
OY 196 KSAQKD-----LOSADKETSLSKKL 216  
DB 900 TDSKKEQDLDLVLLADQDKILSLSKL 927

RESULT 40  
P92021 PRELIMINARY; PRT; 1164 AA.

AC P92021;  
DT 01-NOV-1997 (TREMBlrel. 03, Created)  
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE T10G3.5 PROTEIN.  
GN T10G3.5.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;  
OC Rhabditidae; Peloderinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;

RN [1]  
RP SEQUENCE FROM N.A.  
RA Burton J.;  
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99069613; PubMed=9851916;  
RA none;  
RT "Genome sequence of the nematode C. elegans: A platform for  
RT Investigating biology."  
RL Science 282:2012-2018(1998).  
DR EMBL; Z81118; CAB03330.1;  
DR InterPro; IPR002048; EF-hand.  
DR InterPro; IPR000822; ZnF-C2H2.  
DR InterPro; IPR000306; ZnF\_FYVE.  
DR Pfam; PF01363; FYVE; 1.  
DR SMART; SM00064; FYVE; 1.  
DR SMART; SM00355; ZnF\_C2H2; 1.  
DR PROSITE; PS00018; EF\_HAND; UNKNOWN\_1.  
DR PROSITE; PS00028; ZINC\_FINGER\_C2H2\_1; UNKNOWN\_1.  
SQ SEQUENCE 1164 AA; 135041 MW; 0C8C438680E755C3 CRC64;

Query Match 14.6%; Score 155.5; DB 5; Length 1164;  
Best Local Similarity 24.8%; Pred. No. 0.3;  
Matches 52; Conservative 51; Mismatches 80; Indels 27; Gaps 6;

OY 22 EFLKNELDNVRRAQLSOKDK-----EKRSQYIIDTLRDTL-----EERNATV 63  
DB 700 ELKAYOVEKVSNEISEKQOEVENLMAEMRKKAHWKTRDFEFQOMLRNQNDEASSTL 759  
OY 64 VSLQALGKAKMLCSTLKKOMKYLEQOODETKQAQEAAGRLSRKMKTMEOIELLOSQ 123  
DB 760 KSVQDLKREKETSGEEKNQLISVQLEELKTEVERL--IRSEEEKTOEIEKLSAVTA 817  
OY 124 EVEEMIRDMGVGSAYQQLAVYCVSLKKEYENLKAARKASGEVADKLKDLFSSRSKLQ 183  
DB 818 TTQE--RDELTAAT--ESLRTECNLNSKIOSIESRRHAEKGSENLERNITEKSRLE- 872  
OY 184 VYSELDAQLELKSQDKLQASADKEIMSLK 213  
DB 873 --KDIEERESTIOSIQEALFKDNEIESLK 900

Search completed: September 4, 2002, 16:16:02  
Job time: 1486 sec



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